

genomics@genomics: ~













genomics@genomics:~\$

Introduction to Linux

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NGS WORKSHOP 1403/06/27

Slides based on Sophie Shaw's Slides

Learning Objectives

- Installing Ubuntu Virtual Machine
- 2. Training File and Directory Commands (Terminal)
- 3. Training Viewing and Searching File Commands (Terminal)
- 4. Installing software packages on Ubuntu OS

Watching vs Doing



Listen when you see this cat

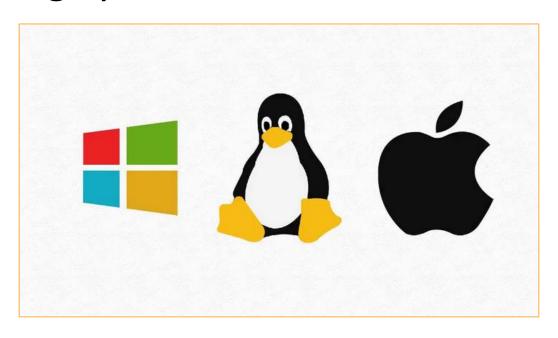


Do when you see this cat



What is Linux?

Operating System



Why Linux?



- Bioinformatics software designed to run on Linux platforms.
- Large amounts of data.
- Much faster than your Windows PC.









Command line interface

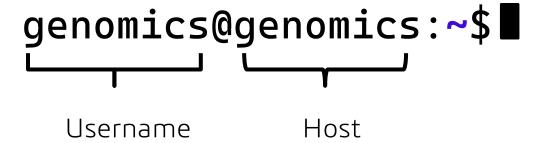




Graphical User Interface (GUI)

Command Line Interface (CLI)

We use these names



Installing Ubuntu Virtual Machine

- 1. Downloading VMware workstation pro 17 and Ubuntu 22
 - 1. https://soft98.ir/os/virtual-machine/1232-vmware-workstation.html
 - 2. https://releases.ubuntu.com/22.04/ubuntu-22.04.5-desktop-amd64.iso
- 2. Installing VMware
- 3. Installing Ubuntu on VMware

Install VMware workstation pro 17



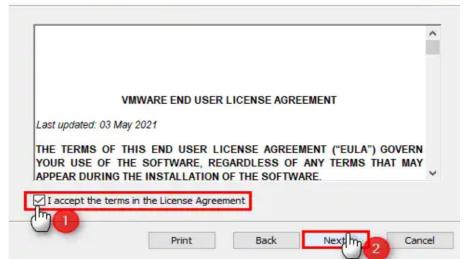


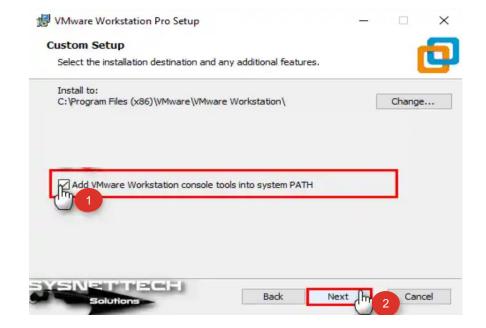


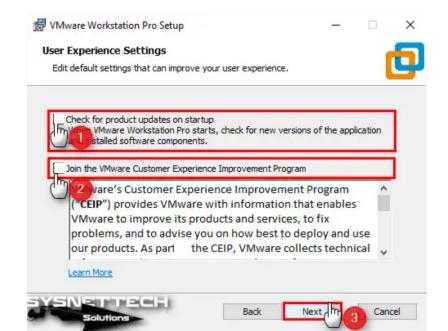
End-User License Agreement

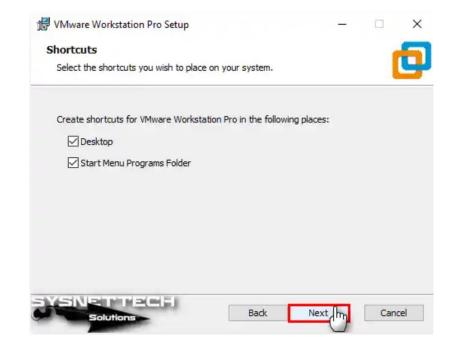
Please read the following license agreement carefully.

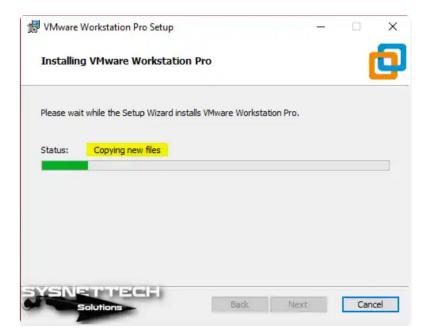


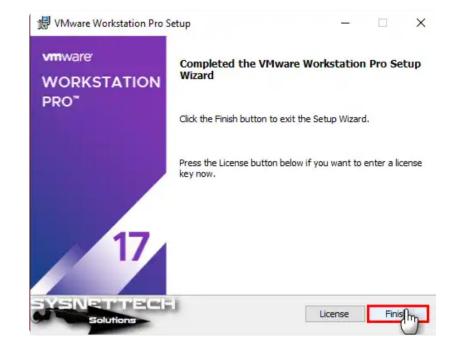














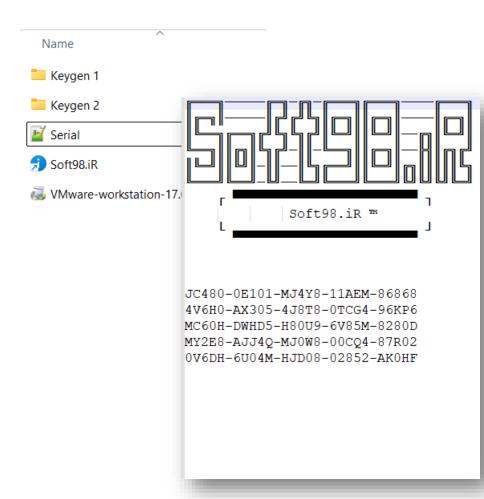
SYSNETTECH

Solutions

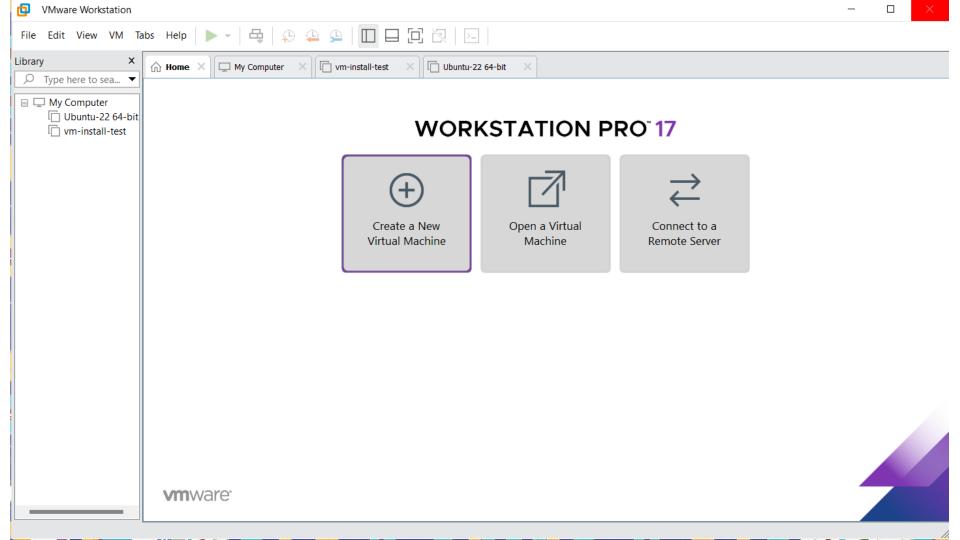
When the PC restarts, double-click the VMware shortcut to open it.

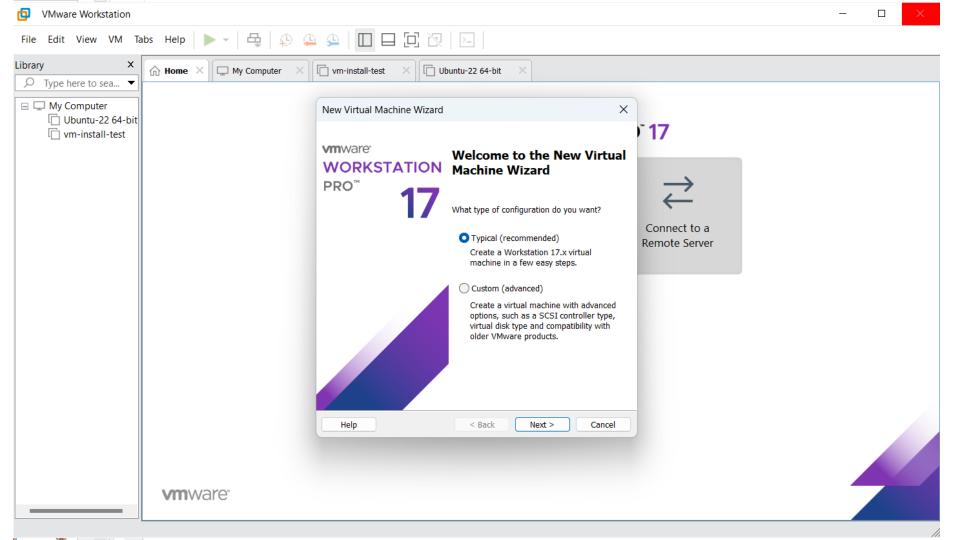


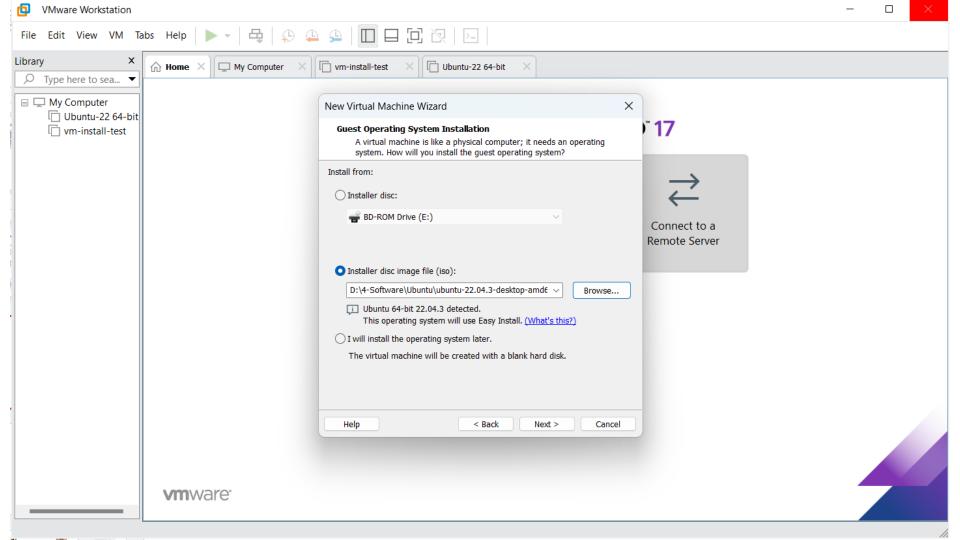


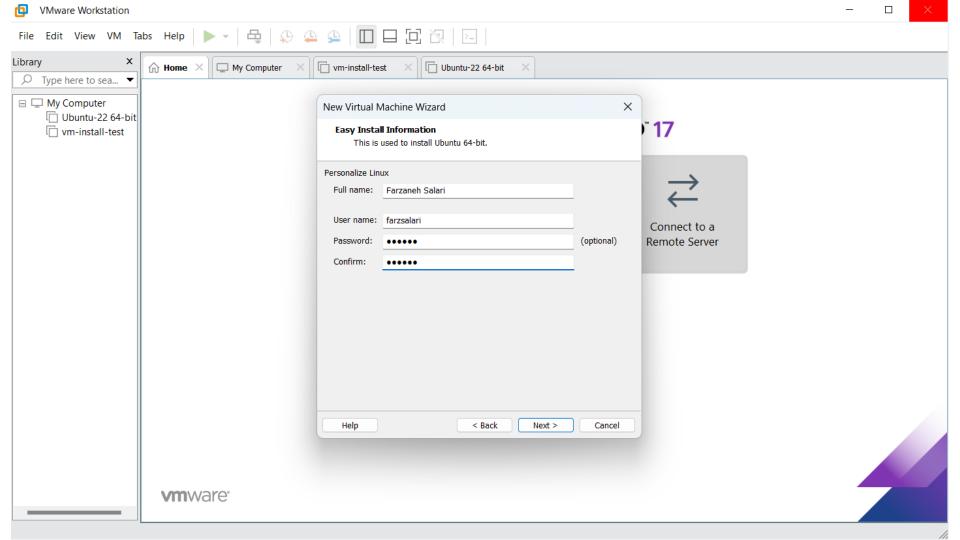


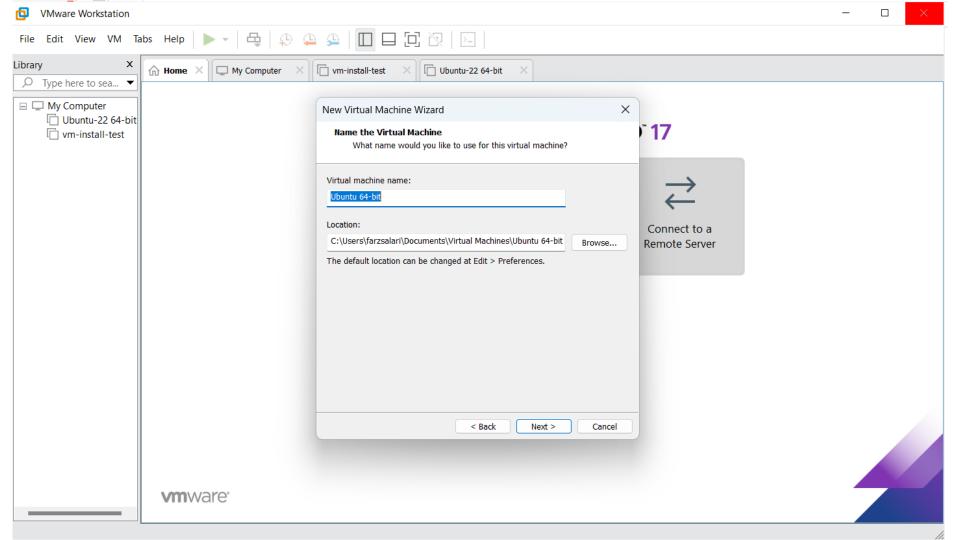
Create a New Virtual Machin

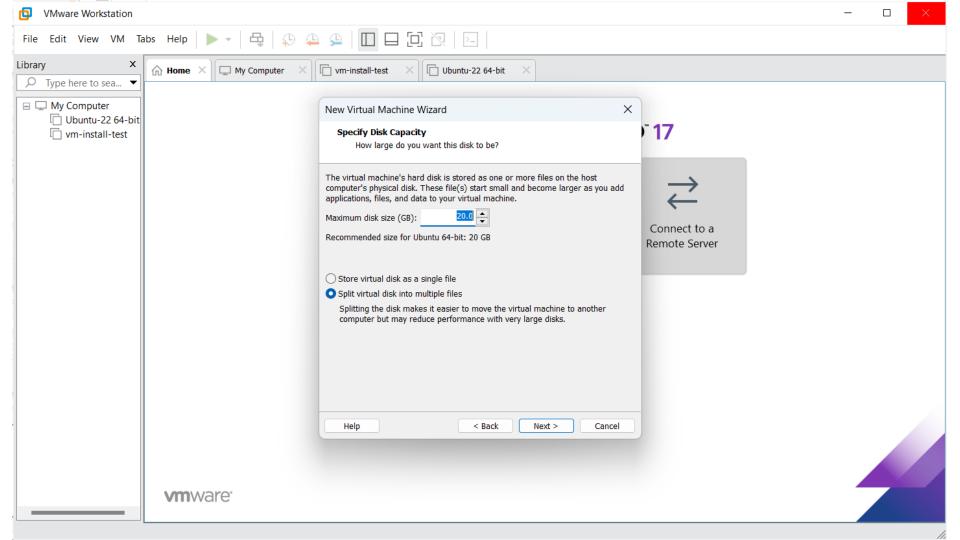


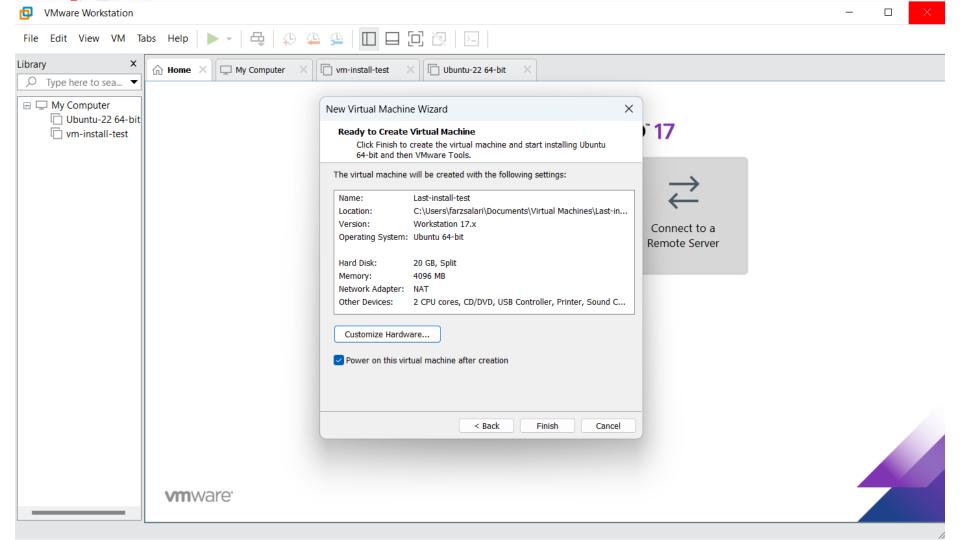


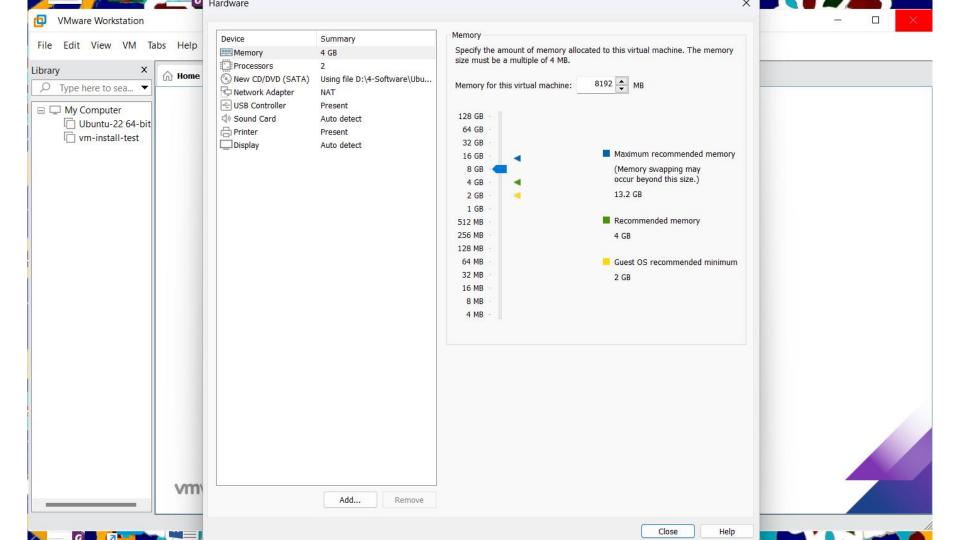




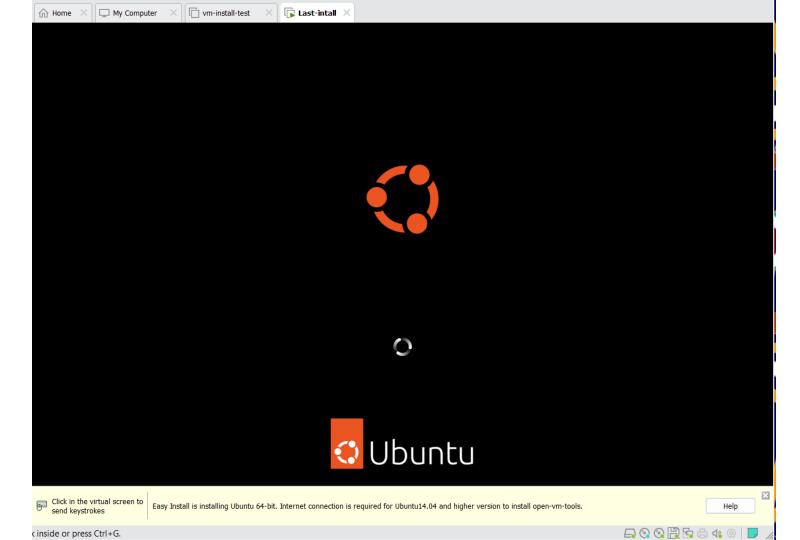


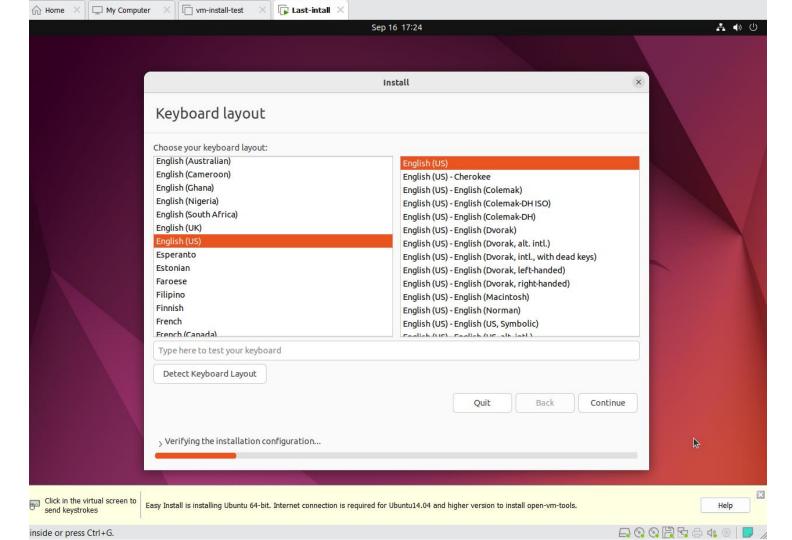


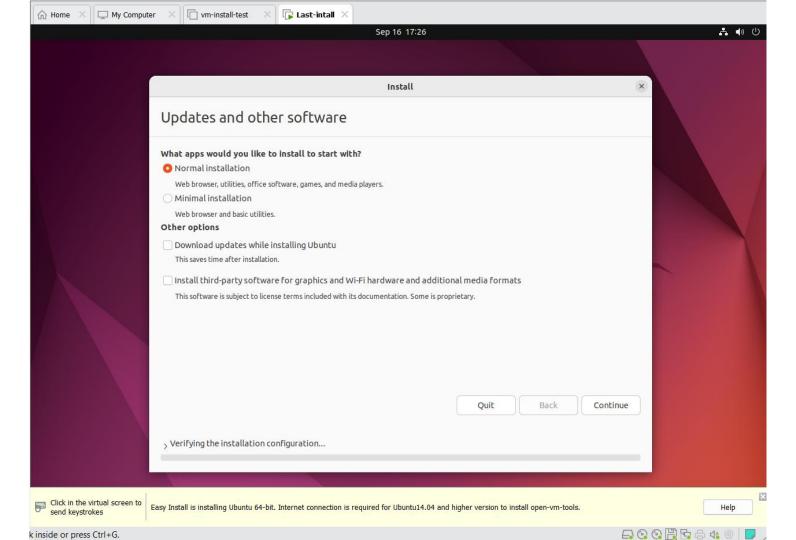


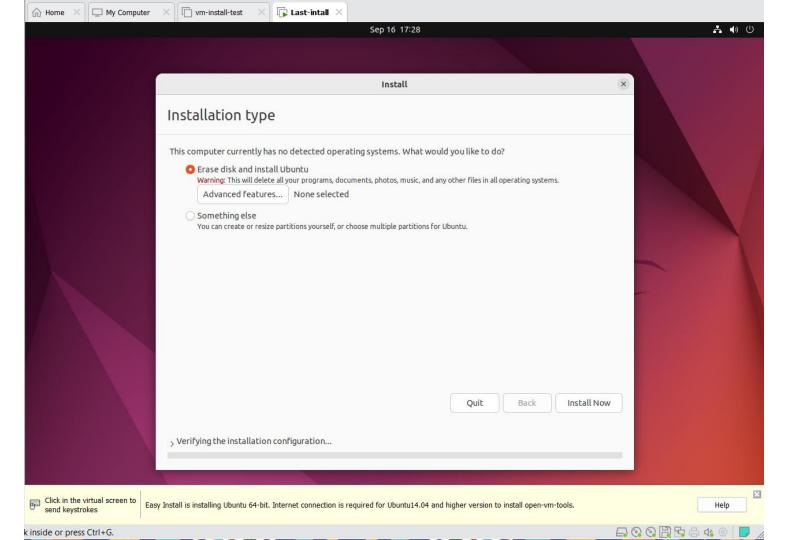


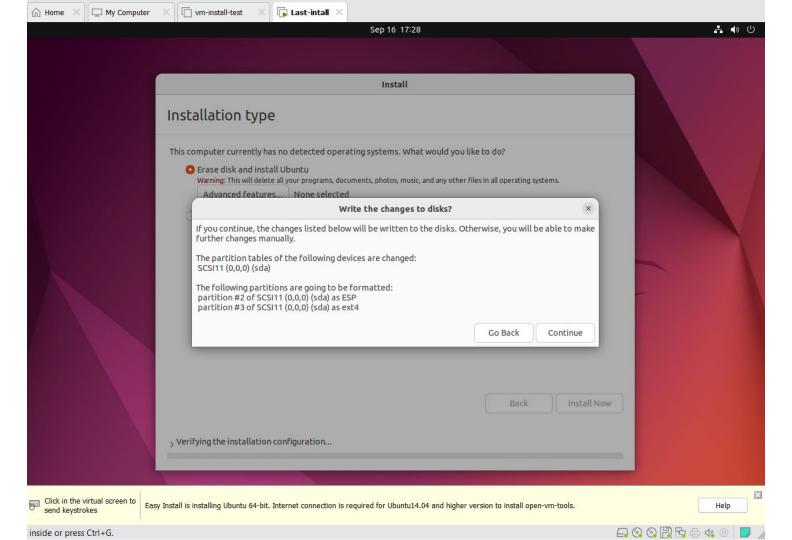
Install Ubuntu 22

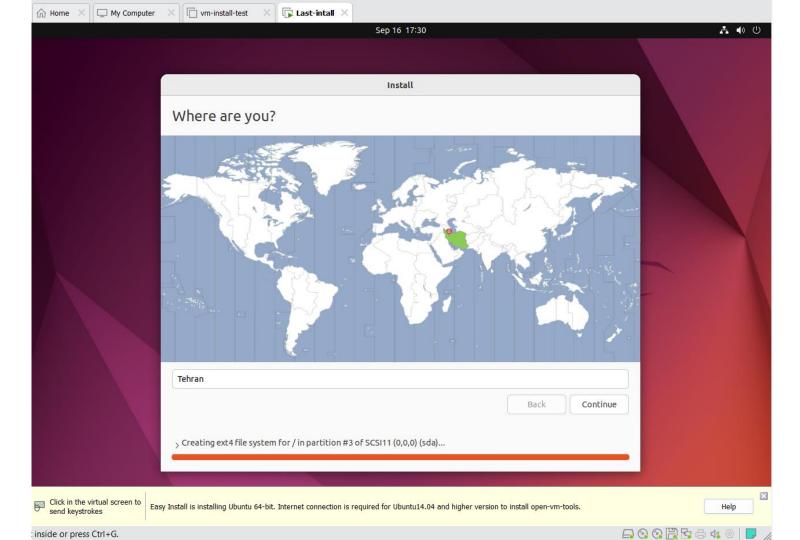


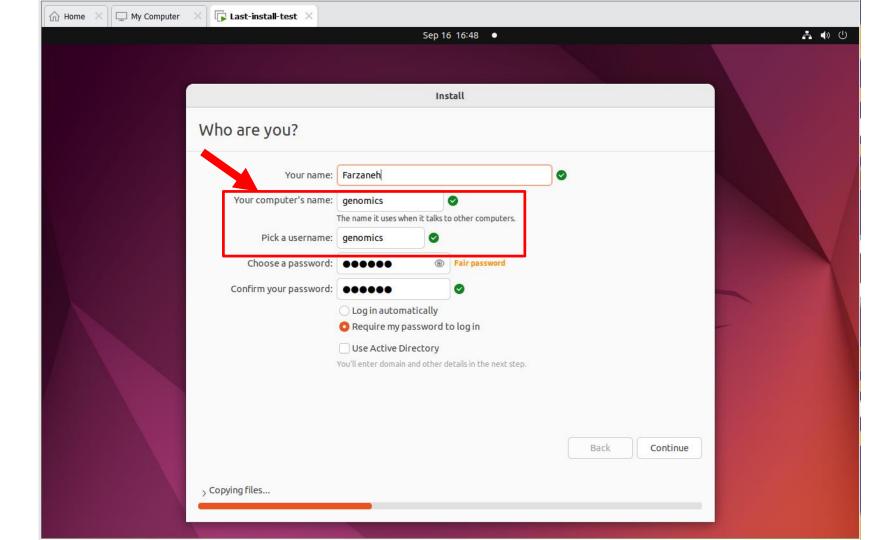


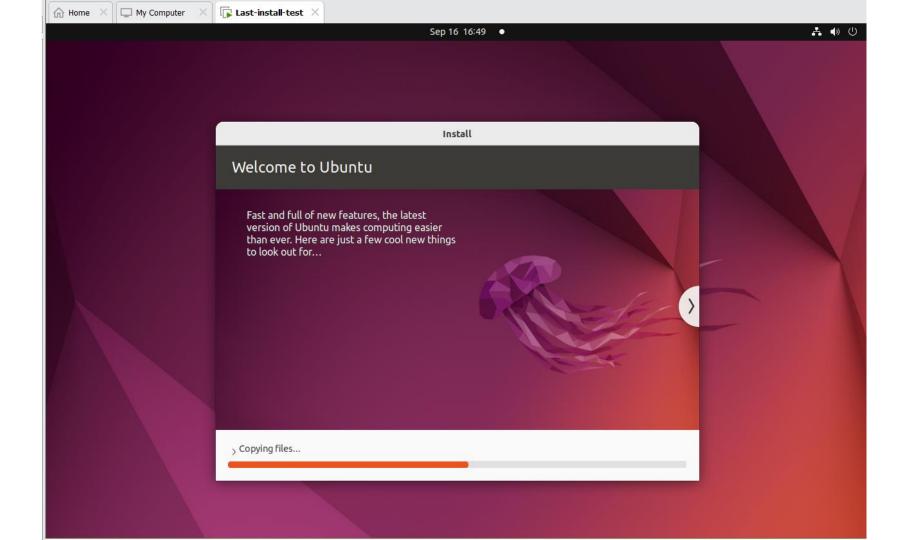






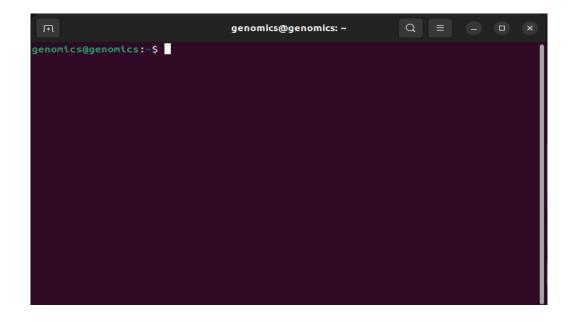






The Terminal





The Command Line, The Shell, The Prompt

Where you see this "\$" followed by text, I want you to type the text on your command line

Unix/Linux Command Reference

File Commands

ls - directory listing

ls -al - formatted listing with hidden files

cd dir - change directory to dir

cd - change to home

pwd - show current directory

mkdir dir - create a directory dir

rm file - delete file

rm -r dir - delete directory dir

rm -f file - force remove file

rm -rf dir - force remove directory dir * cp file1 file2 - copy file1 to file2

cp -r dir1 dir2 - copy dir1 to dir2; create dir2 if it doesn't exist

mv file1 file2 - rename or move file1 to file2 if file2 is an existing directory, moves file1 into directory file2

In -s file link - create symbolic link link to file

touch file - create or update file cat > file - places standard input into file

more file - output the contents of file head file - output the first 10 lines of file

tail file - output the last 10 lines of file tail -f file - output the contents of file as it grows, starting with the last 10 lines

Process Management ps - display your currently active processes

top - display all running processes kill pid - kill process id pid

killall proc - kill all processes named proc * ba - lists stopped or background jobs: resume a stopped job in the background

fg - brings the most recent job to foreground fg n - brings job n to the foreground

File Permissions

chmod octal file - change the permissions of file to octal, which can be found separately for user, group, and world by adding:

 4 - read (r) 2 - write (w)

1 - execute (x)

Examples:

chmod 777 - read, write, execute for all chmod 755 - rwx for owner, rx for group and world For more options, see man chmod.

SSH

ssh user@host - connect to host as user ssh -p port user@host - connect to host on port port as user

ssh-copy-id user@host - add your key to host for user to enable a keved or passwordless login

Searching

grep pattern files - search for pattern in files grep -r pattern dir - search recursively for pattern in dir

command | grep pattern - search for pattern in the output of command

locate file - find all instances of file

System Info

date - show the current date and time

cal - show this month's calendar uptime - show current uptime

w - display who is online

whoami - who you are logged in as

finger user - display information about user

uname -a - show kernel information cat /proc/cpuinfo - cpu information

cat /proc/meminfo - memory information man command - show the manual for command

df - show disk usage

du - show directory space usage free - show memory and swap usage

whereis app - show possible locations of app which app - show which app will be run by default

Compression

tar cf file.tar files - create a tar named file.tar containing files tar xf file.tar - extract the files from file.tar

tar czf file.tar.gz files - create a tar with Gzip compression tar xzf file.tar.gz - extract a tar using Gzip tar cjf file.tar.bz2 - create a tar with Bzip2

compression tar xjf file.tar.bz2 - extract a tar using Bzip2 gzip file - compresses file and renames it to

gzip -d file.gz - decompresses file.gz back to

Network

ping host - ping host and output results

whois domain - get whois information for domain dig domain - get DNS information for domain dig -x host - reverse lookup host

wget file - download file wget -c file - continue a stopped download

Installation

Install from source: ./configure

make

make install

dpkg -i pkg.deb - install a package (Debian) rpm -Uvh pkg.rpm - install a package (RPM)

Shortcuts

Ctrl+C - halts the current command

Ctrl+Z - stops the current command, resume with fg in the foreground or bg in the background

Ctrl+D - log out of current session, similar to exit Ctrl+W - erases one word in the current line

Ctrl+U - erases the whole line

Ctrl+R - type to bring up a recent command

!! - repeats the last command exit - log out of current session

* use with extreme caution.



Terminal Commands

- Run (VM or https://www.terminaltemple.com/)
 - Exploring your current directory
 - Making and changing directories
 - Removing files and directories
- Run (VM or https://sandbox.bio/tutorials/terminal-basics)
 - Viewing and manipulating files
 - Searching files
 - Putting it all together

Location is Important

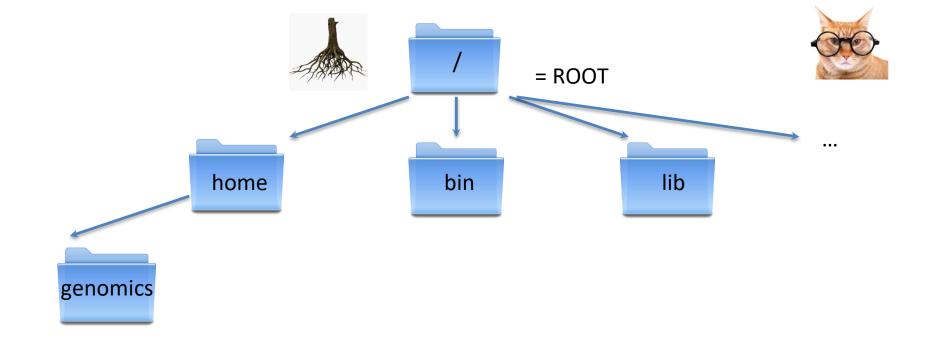


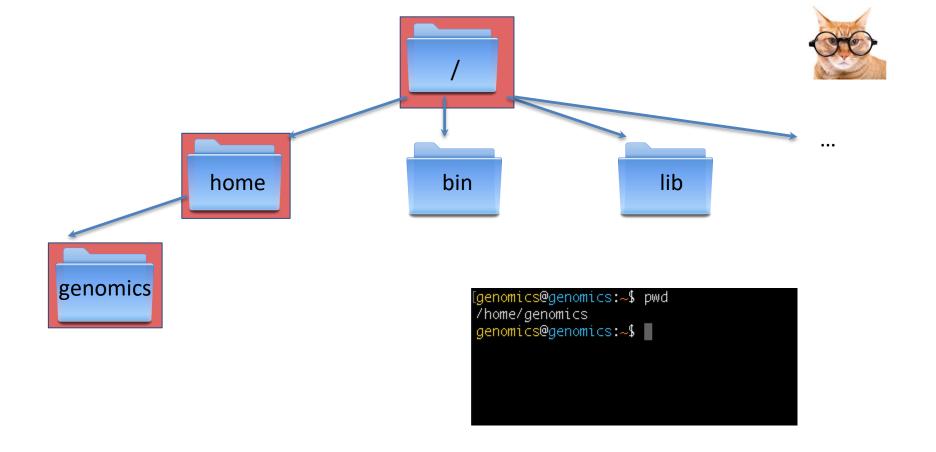
First Task – Where am I?

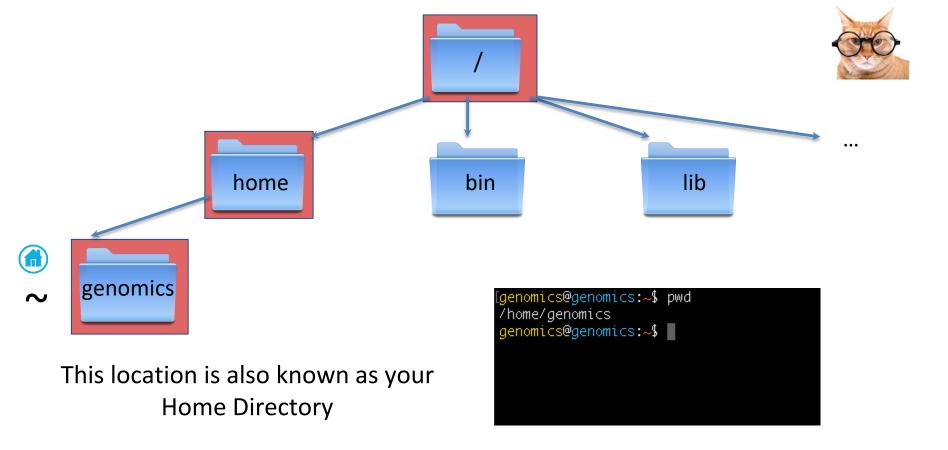
\$ pwd

```
[genomics@genomics:~$ pwd
/home/genomics
genomics@genomics:~$
```

This is your "present working directory".







Tilde is shorthand for Home ~

Now let's create some directories and files



Make a directory

\$ mkdir Data

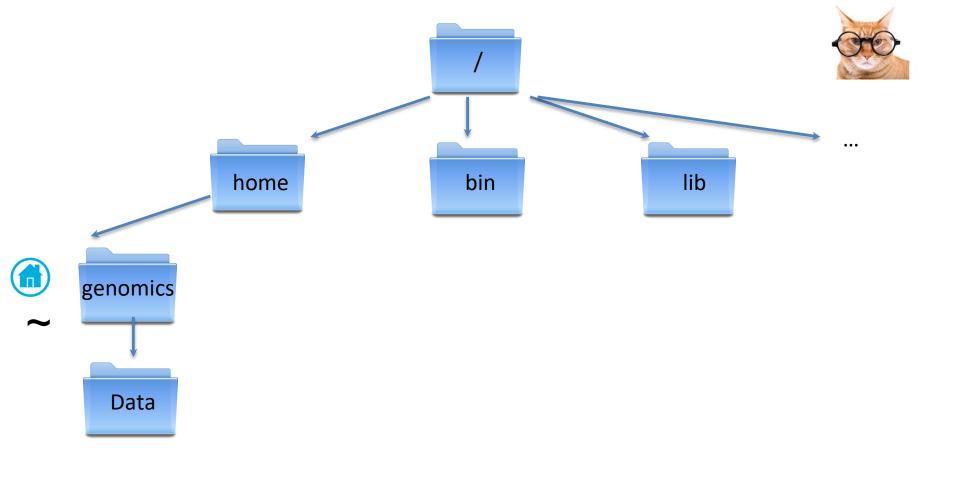
Change into this directory

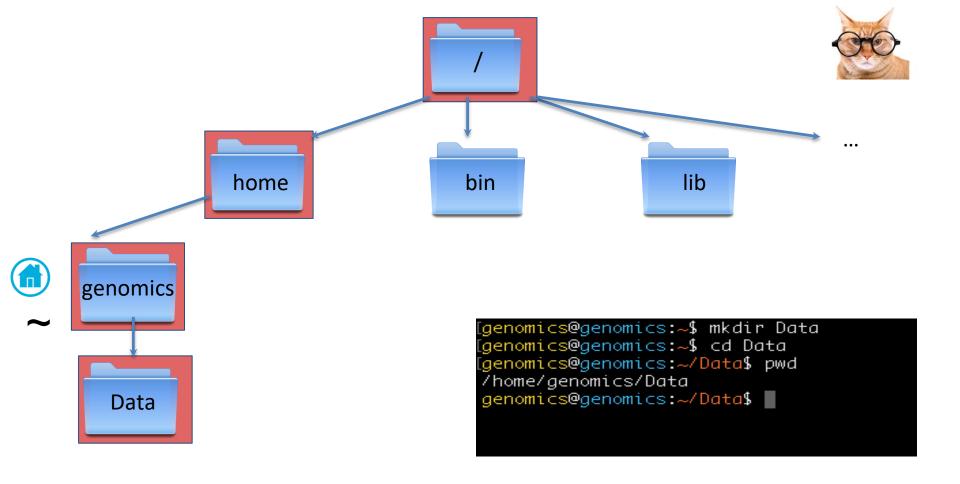
\$ cd Data

Now what is your present working directory?

NOTE! Directory names (and file names for the matter) can not contain spaces.

Underscores are often used instead if you want to separate words.





Now let's create some directories and files



Make an empty file

\$ touch rags

And another two

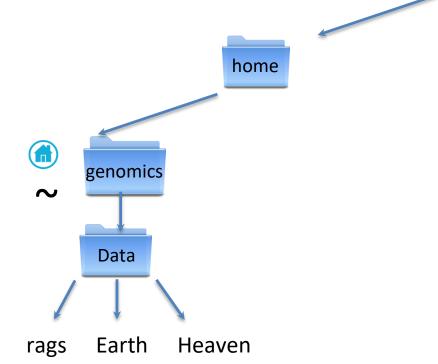
\$ touch Earth

\$ touch Heaven

Now let's list the contents of the current directory (Data)

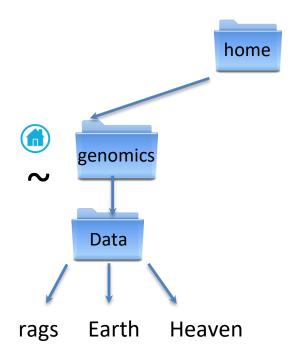
\$ ls

```
genomics@genomics:~/Data$ touch rags
genomics@genomics:~/Data$ touch Earth Heaven
genomics@genomics:~/Data$ ls
Earth Heaven rags
genomics@genomics:~/Data$ |
```







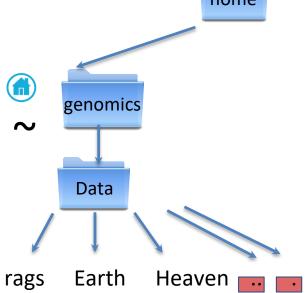


Now list ALL of the files \$ ls -a

```
[genomics@genomics:~/Data$ ls -a
- .. Earth Heaven rags
genomics@genomics:~/Data$ |
```

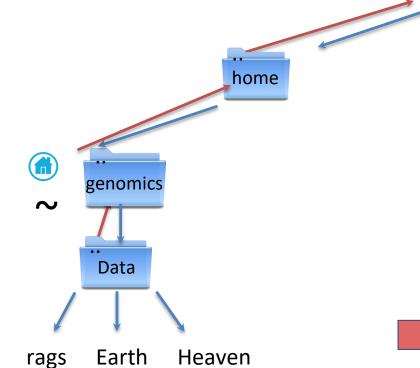






Now list ALL of the files \$ ls -a

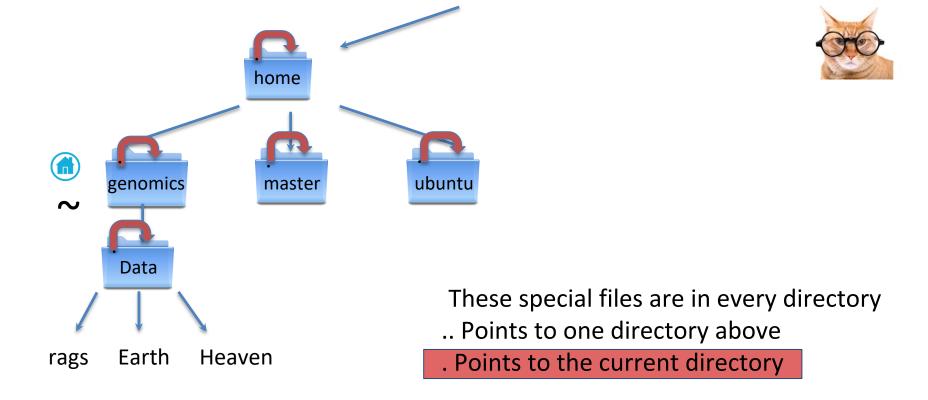
```
[genomics@genomics:~/Data$ ls -a
- .. Earth Heaven rags
genomics@genomics:~/Data$ |
```





These special files are in every directory

- .. Points to one directory above
- . Points to the current directory





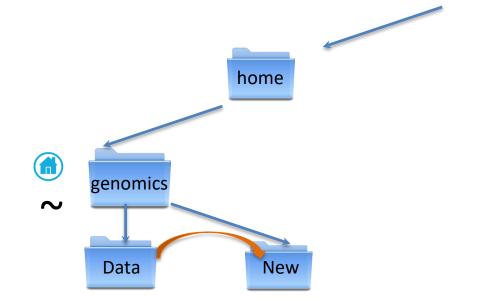


. and .. are used for specifying location

Whenever you do anything on Linux (move around, move a file, rename a file etc...) You have to tell the system where that thing is using a path

. and .. are part of RELATIVE paths



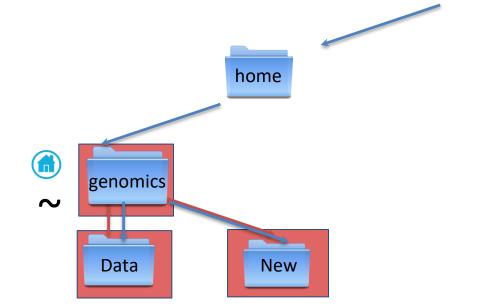




Moving from Data to New

RELATIVE PATH

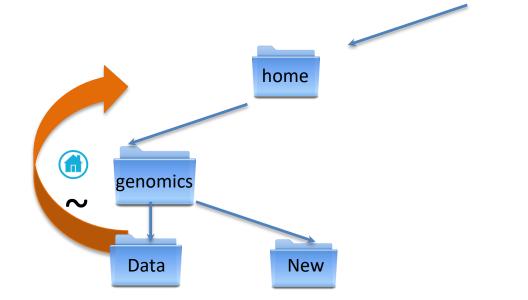
\$ cd ../New





Moving from Data to New

RELATIVE PATH
\$ cd ../New

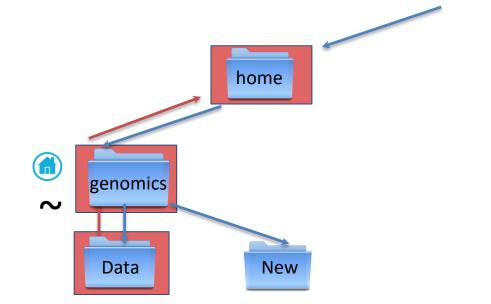




Moving from Data to home

RELATIVE PATH

\$ cd ../../





Moving from Data to home

\$ cd ../../

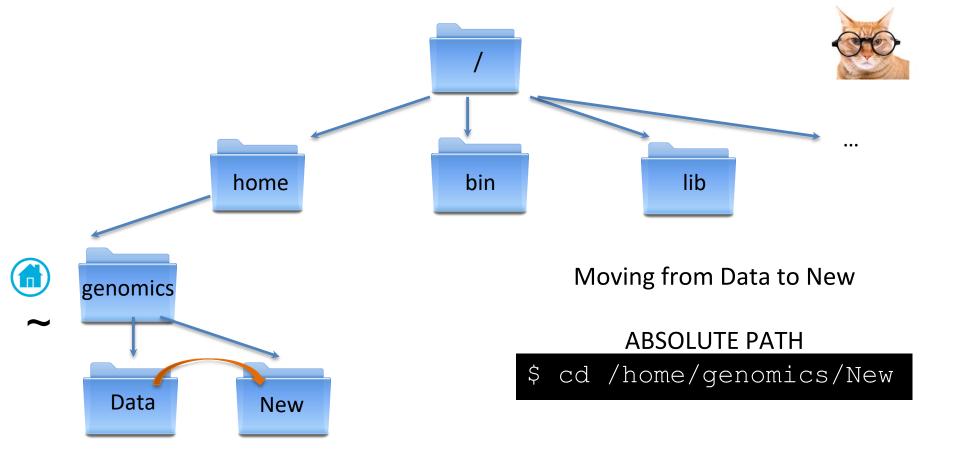


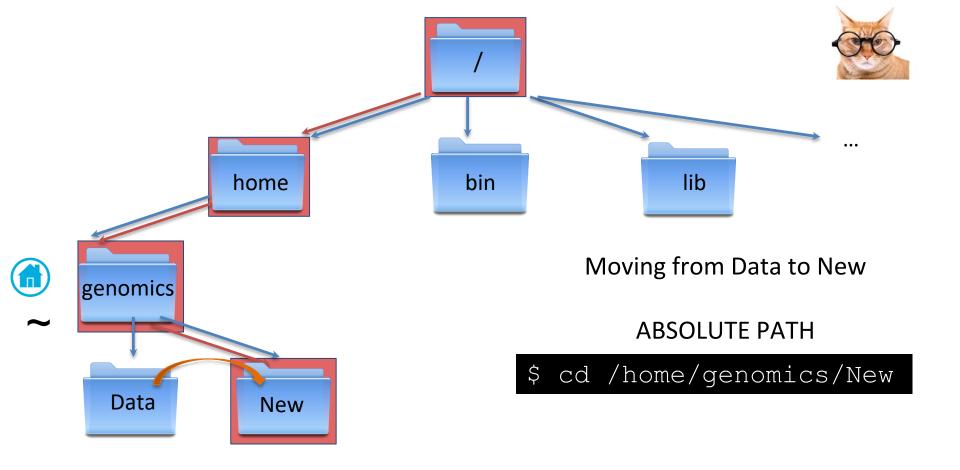


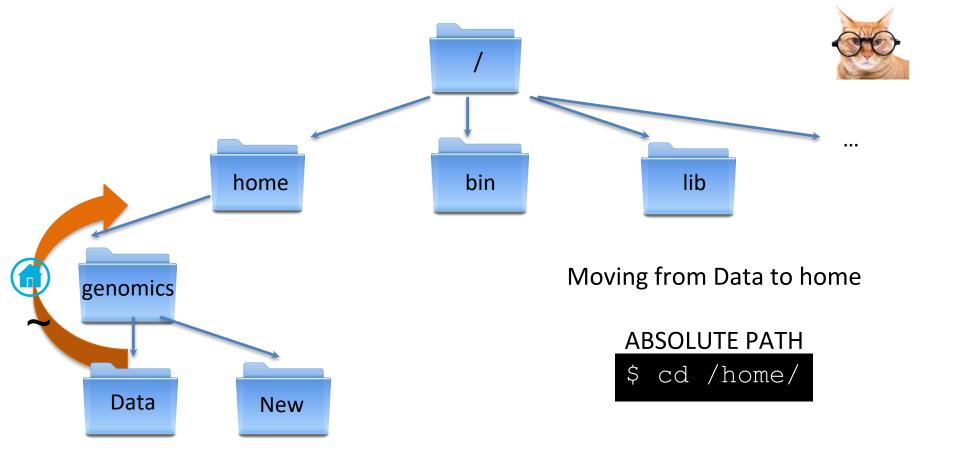
Relative paths will always change depending on your location.

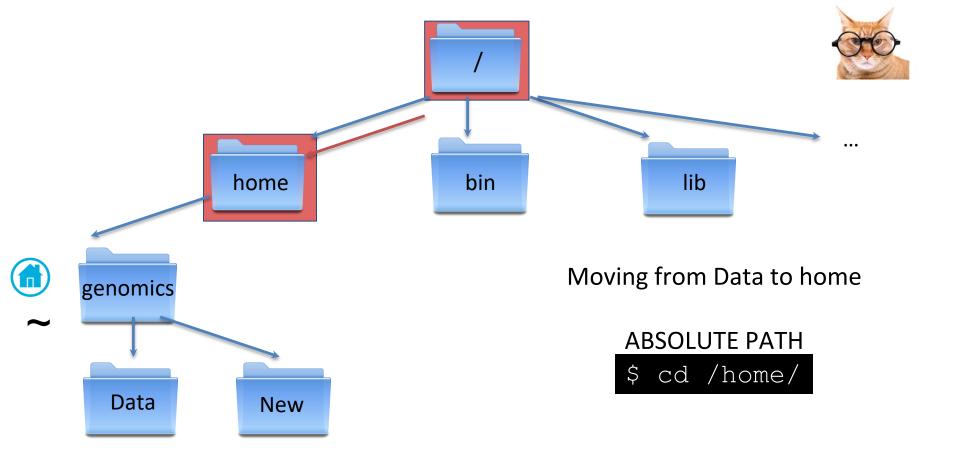
The alternative is ABSOLUTE paths.
These always start from root and will never change.











Let's put this to practice



Where am I right now? (Should be the Data directory)



Change to the directory above

```
$ cd ../
```

Let's list the contents of the Data directory

```
$ ls ./Data/
```

CHALLENGE 1!

- 1. Move into the Data directory and list the contents of your home directory
- 2. In Data, make a new directory and move into this location
- 3. From this new directory, move into your own home directory (genomics) IN ONE COMMAND and check your location

Challenge 1!



1. <u>Move into the</u> Data directory and list the contents of your Home directory

```
$ cd Data
$ ls .. OR $ ls /home/genomics/ OR $ ls ~
```

2. In Data, make a new directory and move into this location

```
$ mkdir new
$ cd new
```

3. From this new directory, move into your Home directory IN ONE COMMAND and check vour location

```
$ cd ../.. OR $ cd /home/genomics/ OR $ cd ~ OR $ cd
$ pwd
```

Any Questions So Far?





Every binary program has a manual



To view the manual page, type man followed by the name of the program





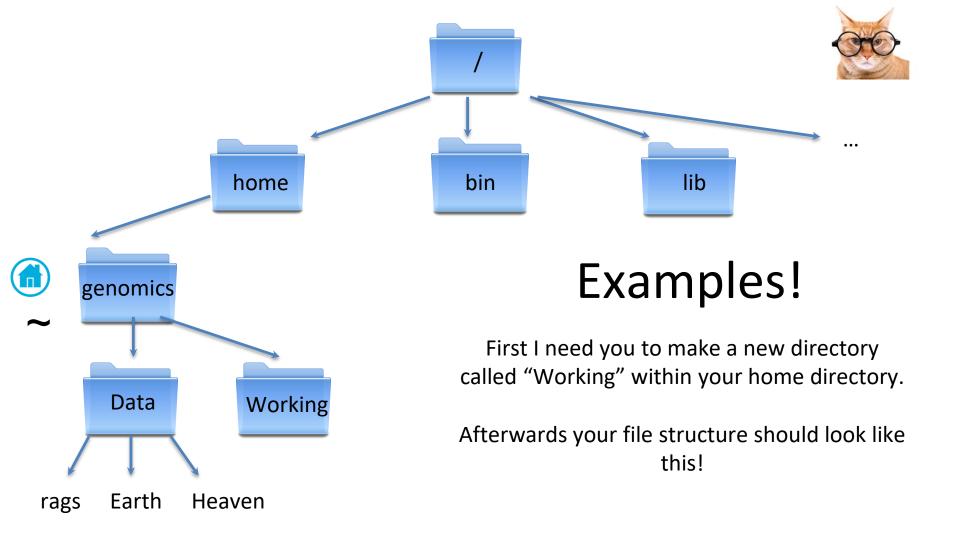
Open the manual page for Is

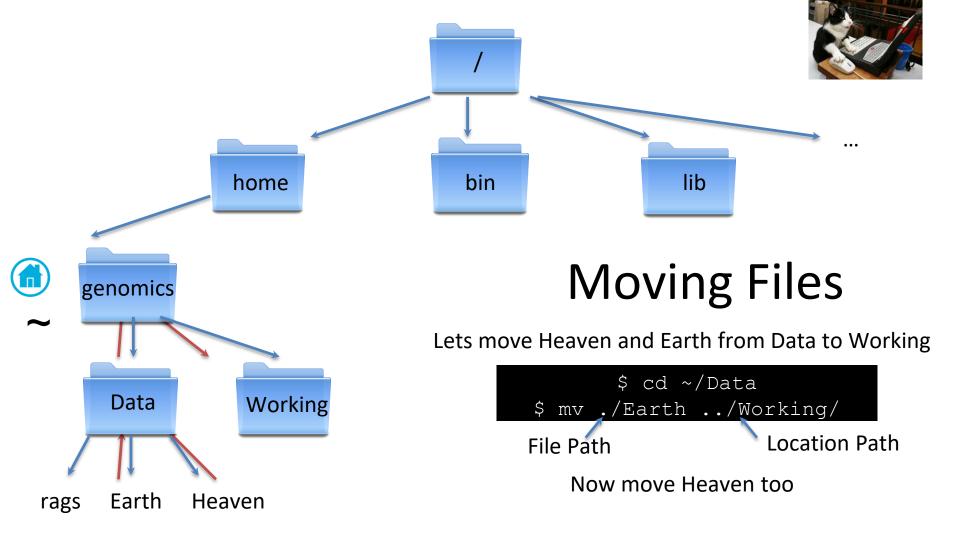


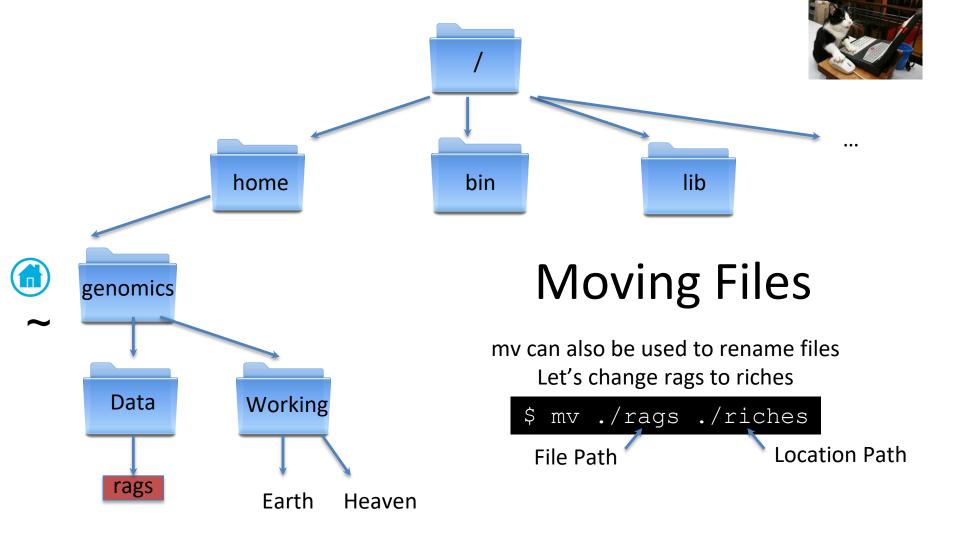
Scroll through (enter) and find the options for:

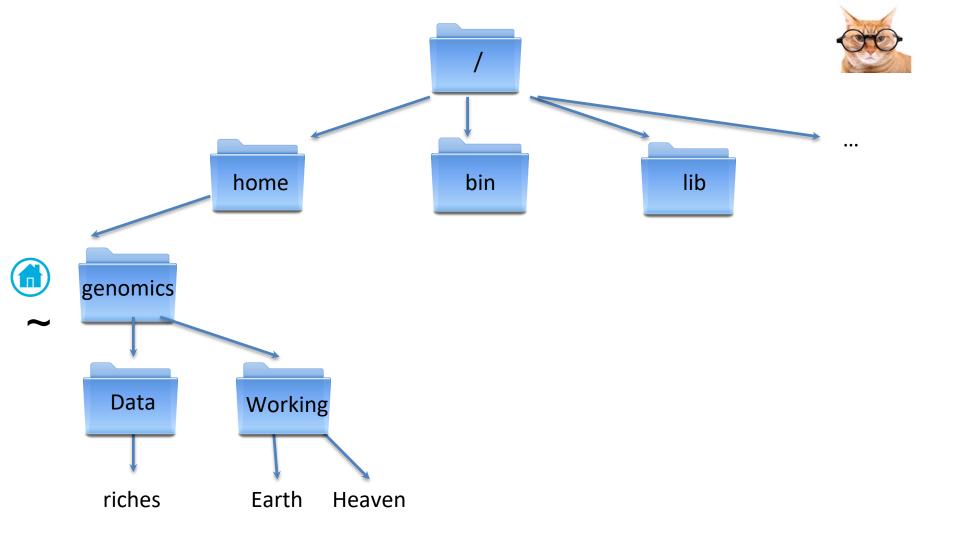
long listing format (-I), human-readable sizes (-h) and sort by modification time (-t)

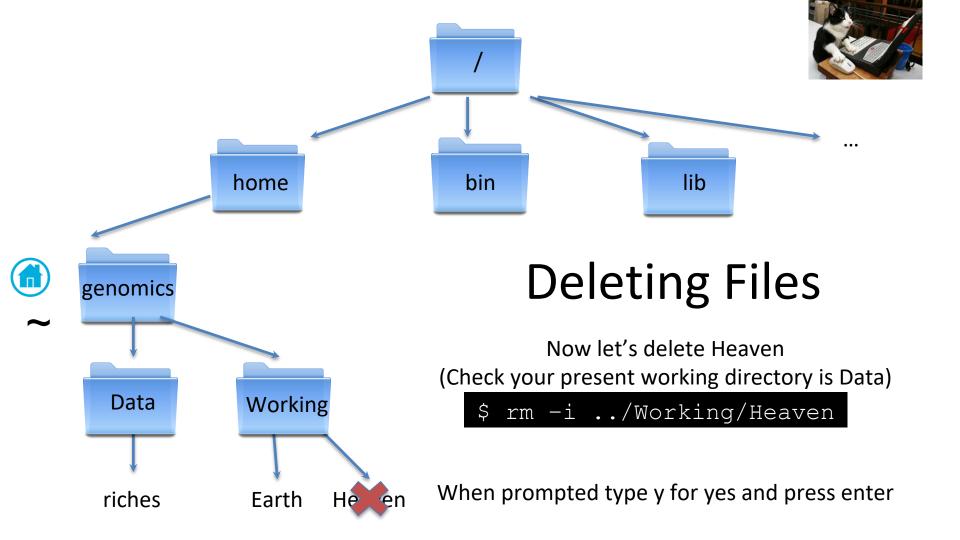
Exit the manual page (type q)

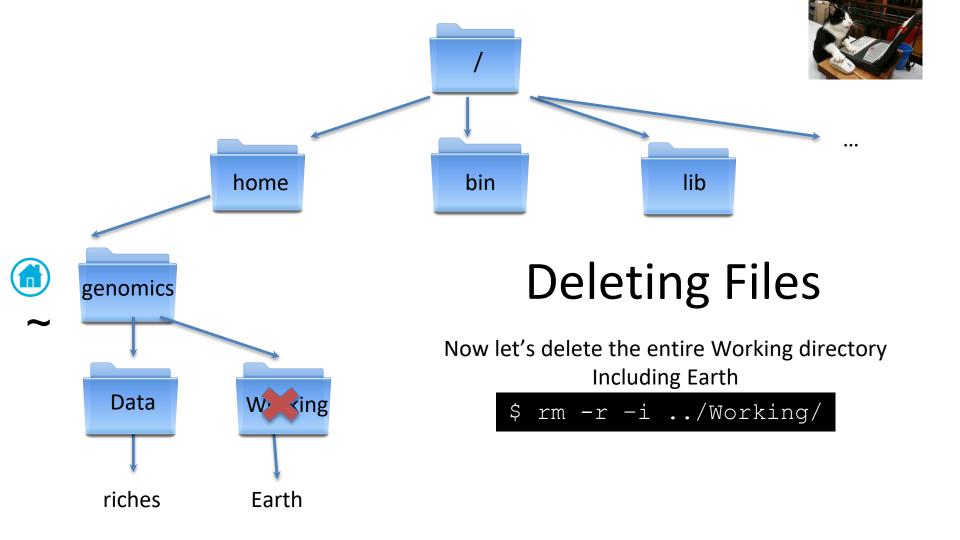


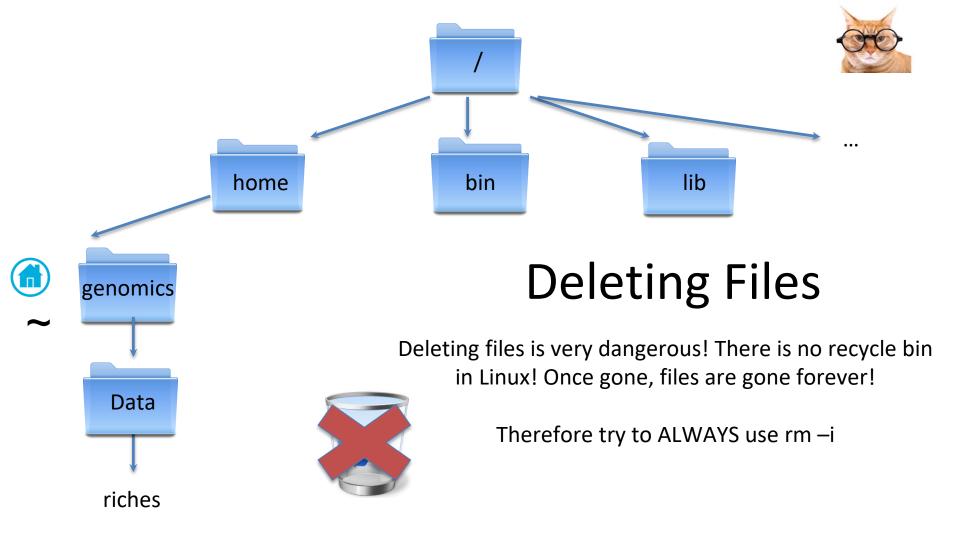


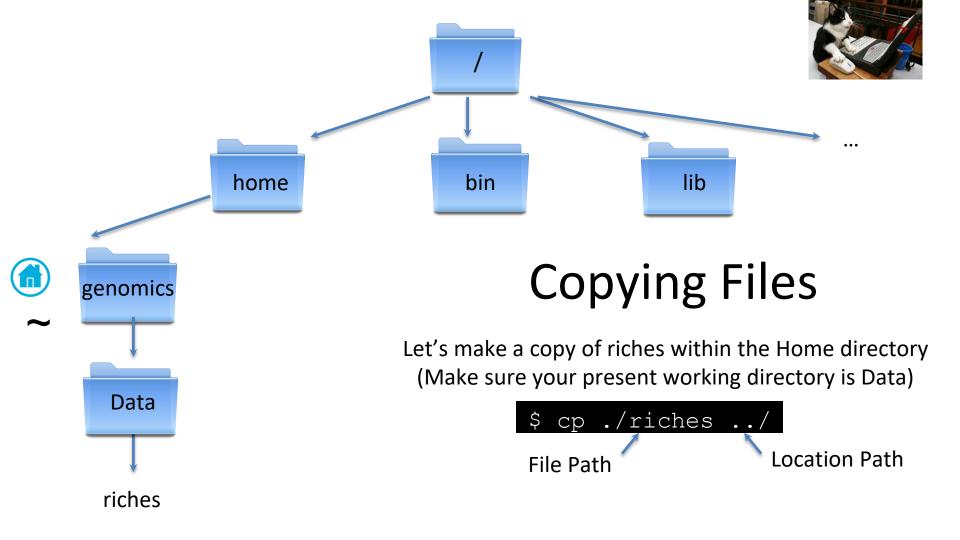


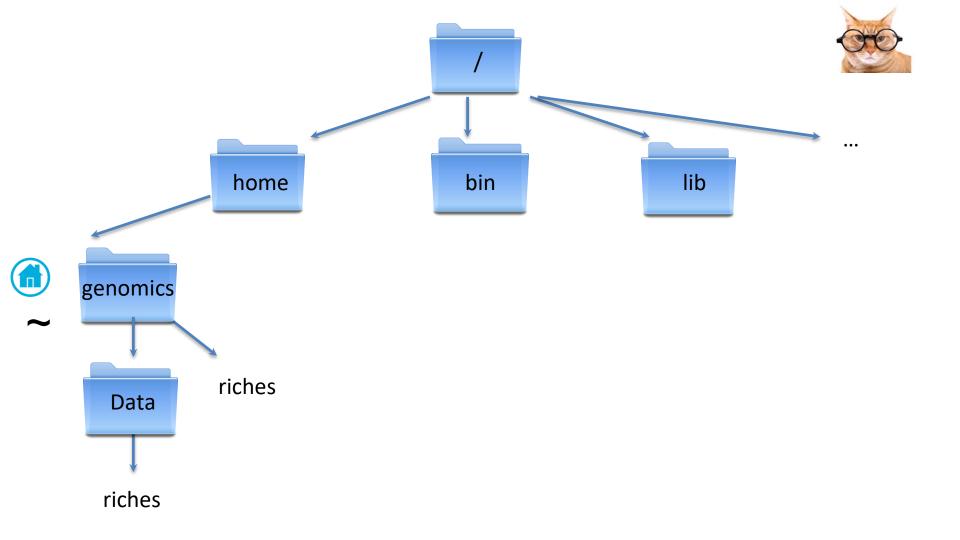


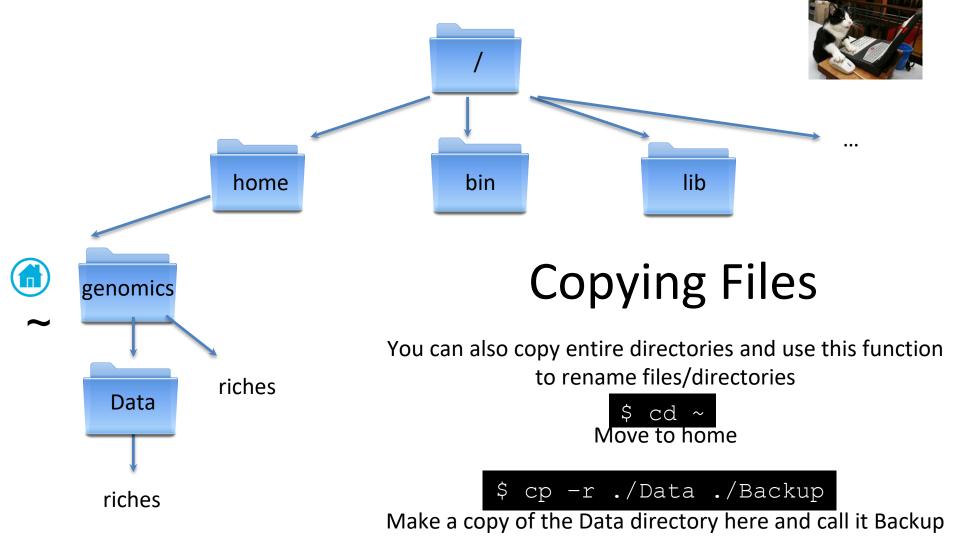


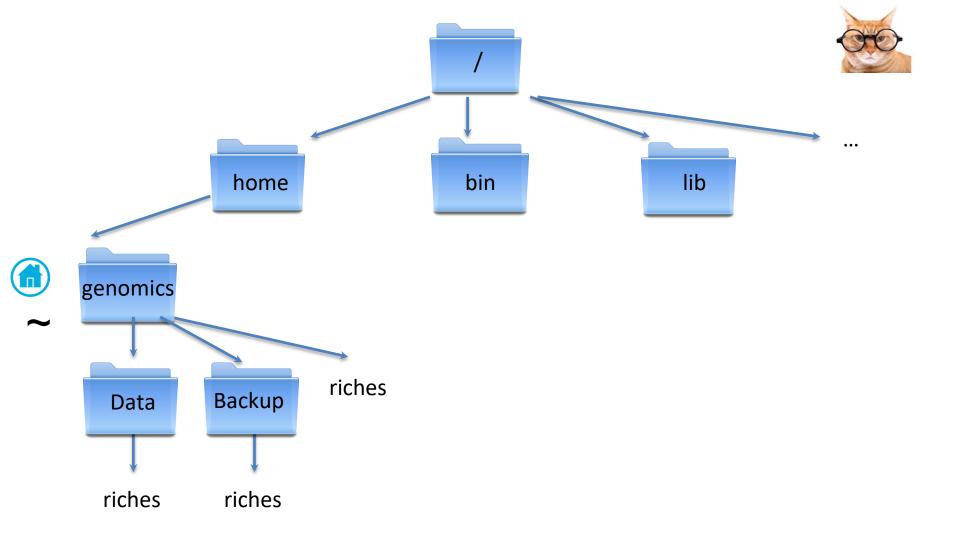












Any Questions So Far?



The End of the second session

```
File Commands
ls - directory listing
ls -al - formatted listing with hidden files
cd dir - change directory to dir
cd - change to home
pwd - show current directory
mkdir dir - create a directory dir
rm file - delete file
rm -r dir - delete directory dir
rm -f file - force remove file
rm -rf dir - force remove directory dir *
cp file1 file2 - copy file1 to file2
cp -r dirl dir2 - copy dir1 to dir2; create dir2 if it
doesn't exist
mv file1 file2 - rename or move file1 to file2
if file2 is an existing directory, moves file1 into
directory file2
In -s file link - create symbolic link link to file
touch file - create or update file
cat > file - places standard input into file
more file - output the contents of file
head file - output the first 10 lines of file
tail file - output the last 10 lines of file
tail -f file - output the contents of file as it
grows, starting with the last 10 lines
```

Terminal Commands

- Run (VM or https://www.terminaltemple.com/)
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Text Editors



These are pieces of software which can be used to edit files.

Think of them as Unix versions of Notepad.

Some have an interactive user interface – E.G. gedit

Some work from within the command line – E.G. nano, vim, emacs







Key Nano Commands



Ctrl + O – This saves the file. You will be asked for a file name. Type the name and press enter.

Ctrl + X – This exits nano. If the file is unsaved, you will be asked at this point if you'd like to save it.

How Do You Install Software?



Some binary programs come with Ubuntu e.g. mkdir, ls etc...

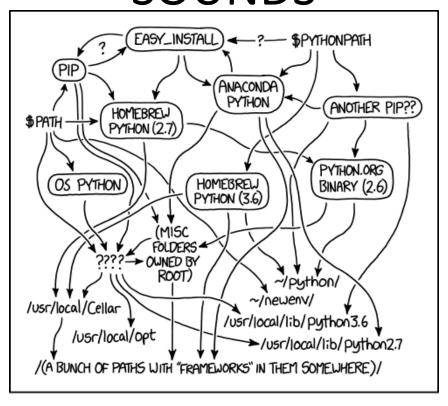
However most software for bioinformatics needs to be installed.

when you begin working on a system you may need to do this.

If you're using a shared compute resource, you'll likely need to ask your system administrator to do this.

IT IS NOT AS EASY AS IT SOUNDS





Software Installation



The "get and compile" method!

Get the software from somewhere and then install it manually.



GitHub is a fantastic repository containing a lot of bioinformatics software! It works using git so it's easy to download.



Challenge 2!

I want you to download and compile the software unicycler.

Here is the github page - https://github.com/rrwick/Unicycler

Make sure you are in your home directory.

Follow the instructions under "Build and run without installation".

Take a read/glance of all of the information under "Requirements" and "Installation" – I just want you to read here!



What Have We Just Done?

```
git clone https://github.com/rrwick/Unicycler.git
```

This has downloaded the software from github

```
cd Unicycler
```

This has changed the location to this new directory

This has COMPILED the software

But what happens if you type unicycler on the command line now?

```
genomics@genomics:~$ unicycler
unicycler: command not found
genomics@genomics:~$
```

Why!? Compiling ≠ Installing!



Installation

For software to be truly installed, it needs to be added to the directory /usr/bin or /usr/local/bin

And this requires admin privileges which you don't have!

However you can still run the newly compiled software directly by using the path:

However! It still won't work...

What! I hear you cry! Why!?

Requirements

- Linux or macOS
- Python 3.4 or later
- C++ compiler with C++14 support:
 - GCC 4.9.1 or later
 - Clang 3.5 or later
 - ICC also works (though I don't know the minimum required version number)
- setuptools (only required for installation of Unicycler)
- For short-read or hybrid assembly:
 - SPAdes v3.6.2 or later (spades.py)
- For long-read or hybrid assembly:
 - Racon (racon)
- For polishing
 - Pilon (pilon1.xx.jar)
 - Java (java)
 - o Bowtie2 (bowtie2-build and bowtie2)
 - Samtools v1.0 or later (samtools)
- For rotating circular contigs:
 - BLAST+ (makeblastdb and tblastn)





A lot of software needs other software to work...
Which in turn needs other software..
Which also needs other software...

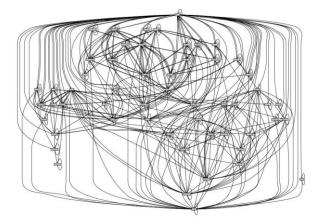


Figure 1.5.: The dependency hell: the runtime dependency graph of Mozilla Firefox

Software Managers



apt install





Important Initial Commands

- 1. sudo apt update
- 2. sudo apt install synaptic
- 3. sudo apt install pip

Confused!?
Don't worry, you
aren't the only one!



This section is just to make you aware of software installation techniques so you aren't surprised when you get home and can't find SAMtools on your system!